L Number	Hits	Search Text	DB	Time stamp
1	0	2002177192-$.did.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:09
2	3	"2002177192"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:10
3	98	Kumar-$.in. AND Rao-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:10
4	2	Kumar-$.in. AND Rao-$.in. AND crystallin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:33
5	9	"552301"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:33
6	5	"5919682"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:33
7	4	"5773245"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:33
8	9	"5561221"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:33
9	36	"4758512"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:34
-	169	(alpha ADJ crystallin) OR (alpha ADJ A ADJ crystallin)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:41
-	112	salerno-j$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:38
-	412	hanna-m$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:38
-	4779	smith-s$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:38
-	4	koretz-j$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:39
-	38666	435/69.1.ccls. OR 435/320.1.ccls. OR 530/350.ccls.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:40
-	61	((alpha ADJ crystallin) OR (alpha ADJ A ADJ crystallin)) AND (435/69.1.ccls. OR 435/320.1.ccls. OR 530/350.ccls.)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:40
-	3	petrash-j$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:41

-	116	petrash-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:41
-	0	petrash-$.in. AND cyrstallin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:41
-	0	griest-t$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 11:42
-	147	(alpha ADJ crystallin) OR (alpha ADJ A ADJ crystallin) AND griest	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/10/21 13:09

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PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	Jul 12	BEILSTEIN enhanced with new display and select options, resulting in a closer connection to BABS
NEWS	4	AUG 02	IFIPAT/IFIUDB/IFICDB reloaded with new search and display fields
NEWS	5	AUG 02	CAplus and CA patent records enhanced with European and Japan Patent Office Classifications
NEWS	6	AUG 02	The Analysis Edition of STN Express with Discover! (Version 7.01 for Windows) now available
NEWS	7	AUG 27	BIOCOMMERCE: Changes and enhancements to content coverage
NEWS	8	AUG 27	BIOTECHABS/BIOTECHDS: Two new display fields added for legal status data from INPADOC
NEWS	9	SEP 01	INPADOC: New family current-awareness alert (SDI) available
NEWS	10	SEP 01	New pricing for the Save Answers for SciFinder Wizard within STN Express with Discover!
NEWS	11	SEP 01	New display format, HITSTR, available in WPIDS/WPINDEX/WPIX
NEWS	12	SEP 27	STANDARDS will no longer be available on STN
NEWS	13	SEP 27	SWETSCAN will no longer be available on STN

NEWS EXPRESS	JULY 30 CURRENT WINDOWS VERSION IS V7.01, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

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* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:18:40 ON 21 OCT 2004

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

```
INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
      AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS,
      BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB,
      CROPU, DDFB, DDFU, DGENE, DISSABS, ...' ENTERED AT 11:18:52 ON 21 OCT 2004

75 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s alpha-crystallin
          5   FILE ADISCTI
          1   FILE ADISNEWS
         49   FILE AGRICOLA
          9   FILE ANABSTR
         17   FILE AQUASCI
          1   FILE BIOBUSINESS
          1   FILE BIOCOMMERCE
          7   FILE BIOENG
       1697   FILE BIOSIS
         15   FILE BIOTECHABS
         15   FILE BIOTECHDS
        689   FILE BIOTECHNO
         56   FILE CABA
         34   FILE CANCERLIT
       1550   FILE CAPLUS
          1   FILE CEABA-VTB
         22   FILE CONFSCI
          7   FILE DDFB
          6   FILE DDFU
         43   FILE DGENE
  27 FILES SEARCHED...
         63   FILE DISSABS
          7   FILE DRUGB
         10   FILE DRUGU
         12   FILE EMBAL
       1528   FILE EMBASE
        400   FILE ESBIOBASE
         23   FILE FEDRIP
          2   FILE FROSTI
          5   FILE FSTA
        688   FILE GENBANK
         18   FILE IFIPAT
         66   FILE JICST-EPLUS
          1   FILE KOSMET
        266   FILE LIFESCI
       1215   FILE MEDLINE
          3   FILE NIOSHTIC
          4   FILE NTIS
          4   FILE OCEAN
        350   FILE PASCAL
  58 FILES SEARCHED...
          8   FILE PROMT
       1500   FILE SCISEARCH
        351   FILE TOXCENTER
        134   FILE USPATFULL
          2   FILE USPAT2
         19   FILE WPIDS
         19   FILE WPINDEX

  46 FILES HAVE ONE OR MORE ANSWERS,   75 FILES SEARCHED IN STNINDEX
```

```
L1   QUE ALPHA-CRYSTALLIN

=> d rank
F1        1697   BIOSIS
F2        1550   CAPLUS
F3        1528   EMBASE
F4        1500   SCISEARCH
F5        1215   MEDLINE
F6         689   BIOTECHNO
F7         688   GENBANK
F8         400   ESBIOBASE
F9         351   TOXCENTER
F10        350   PASCAL
F11        266   LIFESCI
F12        134   USPATFULL
F13         66   JICST-EPLUS
F14         63   DISSABS
F15         56   CABA
F16         49   AGRICOLA
F17         43   DGENE
F18         34   CANCERLIT
F19         23   FEDRIP
F20         22   CONFSCI
F21         19   WPIDS
F22         19   WPINDEX
F23         18   IFIPAT
F24         17   AQUASCI
F25         15   BIOTECHABS
F26         15   BIOTECHDS
F27         12   EMBAL
F28         10   DRUGU
F29          9   ANABSTR
F30          8   PROMT
F31          7   BIOENG
F32          7   DDFB
F33          7   DRUGB
F34          6   DDFU
F35          5   ADISCTI
F36          5   FSTA
F37          4   NTIS
F38          4   OCEAN
F39          3   NIOSHTIC
F40          2   FROSTI
F41          2   USPAT2
F42          1   ADISNEWS
F43          1   BIOBUSINESS
F44          1   BIOCOMMERCE
F45          1   CEABA-VTB
F46          1   KOSMET


=> file f1, f2, f3, f4, f5, f6, f9
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                1.14       1.35

FILE 'BIOSIS' ENTERED AT 11:20:17 ON 21 OCT 2004
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FILE 'SCISEARCH' ENTERED AT 11:20:17 ON 21 OCT 2004

FILE 'MEDLINE' ENTERED AT 11:20:17 ON 21 OCT 2004

FILE 'BIOTECHNO' ENTERED AT 11:20:17 ON 21 OCT 2004

FILE 'TOXCENTER' ENTERED AT 11:20:17 ON 21 OCT 2004


```
=> s alpha-crystallin
L2        8530 ALPHA-CRYSTALLIN

=> s jaworski/au
L3           1 JAWORSKI/AU

=> d l3 ibib ti abs

L3   ANSWER 1 OF 1  EMBASE  COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
ACCESSION NUMBER:    97126859  EMBASE
DOCUMENT NUMBER:     1997126859
TITLE:               Erratum: (The Journal of Cell Biology (April 1994) 125:2
                     (495-509)).
AUTHOR:              Jaworski
SOURCE:              Journal of Cell Biology, (1997) 137/2 (521).
                     ISSN: 0021-9525  CODEN: JCLBA3
COUNTRY:             United States
DOCUMENT TYPE:       Journal; Errata
FILE SEGMENT:        029     Clinical Biochemistry
LANGUAGE:            English
TI   Erratum: (The Journal of Cell Biology (April 1994) 125:2 (495-509)).


=> s l2 and jaworski
L4           0 L2 AND JAWORSKI

=> s alpha-a-crystallin
L5        2161 ALPHA-A-CRYSTALLIN

=> s l5 and jaworski
L6           1 L5 AND JAWORSKI

=> d l6 ibib ti abs

L6   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:        1994:673440  CAPLUS
DOCUMENT NUMBER:         121:273440
TITLE:                   A partial cDNA sequence corrects the human .
                         alpha.A-crystallin primary
                         structure
AUTHOR(S):               Caspers, Gert-Jan; Pennings, Jeroen; De Jong, Wilfried
                         W.
CORPORATE SOURCE:        Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB,
                         Neth.
SOURCE:                  Experimental Eye Research (1994), 59(1), 125-6
                         CODEN: EXERA6; ISSN: 0014-4835
DOCUMENT TYPE:           Journal
```

LANGUAGE: English

TI A partial cDNA sequence corrects the human **.alpha.A-crystallin** primary structure

AB The primary structure of the human **.alpha.A-crystallin** chain was proposed almost 20 yr ago, on the basis of peptide compns. and partial Edman degradation (de Jong et al., 1975; Kramps et al., 1978). With the advent of the DNA era, the largest part of the amino acid sequence was fully confirmed by deduction from the DNA sequences of the first two exons and the 3' end of the third exon of the human **.alpha.A-crystallin** gene (McDevitt et al., 1986; **Jaworski** and Piatigorsky, 1989). The DNA sequence of the larger part of the third exon, corresponding to positions 105-165 in the 173-residue **.alpha.A-crystallin** chain, still remained undetd. During the course of comparative studies of the **.alpha.A-crystallin** sequences of different animals, we designed two degenerate oligonucleotide primers, encompassing a region coding for amino acids 74-160. These primers were used to amplify a partial **.alpha.A-crystallin** cDNA sequence from a human lens cDNA library in phage λgt11 by the polymerase chain reaction (PCR) method (Saiki et al., 1985). PCR products were cloned and the sequence was determined by the dideoxynucleotide chain-termination method. The part of the nucleotide sequence of the human **.alpha.A-crystallin** cDNA that codes for amino acids 105-160 and its derived amino acid sequence were determined

=> d l6 all

L6 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1994:673440 CAPLUS

DN 121:273440

ED Entered STN: 10 Dec 1994

TI A partial cDNA sequence corrects the human **.alpha.A-crystallin** primary structure

AU Caspers, Gert-Jan; Pennings, Jeroen; De Jong, Wilfried W.

CS Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB, Neth.

SO Experimental Eye Research (1994), 59(1), 125-6
CODEN: EXERA6; ISSN: 0014-4835

DT Journal

LA English

CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 13

AB The primary structure of the human **.alpha.A-crystallin** chain was proposed almost 20 yr ago, on the basis of peptide compns. and partial Edman degradation (de Jong et al., 1975; Kramps et al., 1978). With the advent of the DNA era, the largest part of the amino acid sequence was fully confirmed by deduction from the DNA sequences of the first two exons and the 3' end of the third exon of the human **.alpha.A-crystallin** gene (McDevitt et al., 1986; **Jaworski** and Piatigorsky, 1989). The DNA sequence of the larger part of the third exon, corresponding to positions 105-165 in the 173-residue **.alpha.A-crystallin** chain, still remained undetd. During the course of comparative studies of the **.alpha.A-crystallin** sequences of different animals, we designed two degenerate oligonucleotide primers, encompassing a region coding for amino acids 74-160. These primers were used to amplify a partial **.alpha.A-crystallin** cDNA sequence from a human lens cDNA library in phage λgt11 by the polymerase chain reaction (PCR) method (Saiki et al., 1985). PCR products were cloned and the sequence was determined by the dideoxynucleotide chain-termination method. The part of the nucleotide sequence of the human **.alpha.A-crystallin** cDNA that codes for amino acids 105-160 and its derived amino acid sequence were determined

ST human alphaAcrystallin sequence correction partial cDNA
IT Gene, animal
RL: BIOL (Biological study)
(a partial cDNA sequence corrects the human α **A-crystallin** primary structure)
IT Protein sequences
(partial, of α **A-crystallin** of human)
IT Deoxyribonucleic acid sequences
(complementary, partial, for α **A-crystallin** of human)
IT Crystallins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(αA-, a partial cDNA sequence corrects the human α **A-crystallin** primary structure)
IT 158856-54-3
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(corrected amino acid sequence of)
IT 157574-40-8, GenBank L25781
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(corrected nucleotide sequence of)

=> FIL REGISTRY

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	29.38	30.73

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.40	-1.40

FILE 'REGISTRY' ENTERED AT 11:23:52 ON 21 OCT 2004

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STRUCTURE FILE UPDATES: 20 OCT 2004 HIGHEST RN 766487-31-4
DICTIONARY FILE UPDATES: 20 OCT 2004 HIGHEST RN 766487-31-4

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html

=> S 158856-54-3/RN

L7 1 158856-54-3/RN

=> SET NOTICE 1 DISPLAY

NOTICE SET TO 1 U.S. DOLLAR FOR DISPLAY COMMAND

SET COMMAND COMPLETED

=> D L7 SQIDE 1-

YOU HAVE REQUESTED DATA FROM 1 ANSWERS - CONTINUE? Y/(N):y
THE ESTIMATED COST FOR THIS REQUEST IS 5.92 U.S. DOLLARS
DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:y

L7 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN **158856-54-3** REGISTRY
CN α-Crystallin (human A-chain reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN αA-Crystallin (CRYA1) (human clone KB2007G4 gene CRYAA)
CN αA-Crystallin (human eye lens)
CN Crystallin, αA- (human 173-amino acids)
FS PROTEIN SEQUENCE
SQL 173

SEQ 1 MDVTIQHPWF KRTLGPFYPS RLFDQFFGEG LFEYDLLPFL SSTISPYYRQ
51 SLFRTVLDSG ISEVRSDRDK FVIFLDVKHF SPEDLTVKVQ DDFVEIHGKH
101 NERQDDHGYI SREFHRRYRL PSNVDQSALS CSLSADGMLT FCGPKIQTGL
151 DATHAERAIP VSREEKPTSA PSS

RELATED SEQUENCES AVAILABLE WITH SEQLINK
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER
DT.CA CAplus document type: Journal
RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);
PROC (Process); PRP (Properties)
5 REFERENCES IN FILE CA (1907 TO DATE)
5 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> SET NOTICE LOGIN DISPLAY

NOTICE SET TO OFF FOR DISPLAY COMMAND
SET COMMAND COMPLETED

=>

=> FIL REGISTRY

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	6.34	37.07

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-1.40

FILE 'REGISTRY' ENTERED AT 11:24:41 ON 21 OCT 2004
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provided by InfoChem.

STRUCTURE FILE UPDATES: 20 OCT 2004 HIGHEST RN 766487-31-4
DICTIONARY FILE UPDATES: 20 OCT 2004 HIGHEST RN 766487-31-4

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html

=> SET TERMSET E#

SET COMMAND COMPLETED

=> DEL SEL Y

=> SEL L7 1 RN

E1 THROUGH E1 ASSIGNED

=> S E1/RN

L8 1 158856-54-3/RN

=> SET TERMSET LOGIN

SET COMMAND COMPLETED

=> FIL CAPLUS

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.50	37.57

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-1.40

FILE 'CAPLUS' ENTERED AT 11:24:45 ON 21 OCT 2004
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FILE COVERS 1907 - 21 Oct 2004 VOL 141 ISS 17
FILE LAST UPDATED: 20 Oct 2004 (20041020/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=>  S L8

L9            5 L8

=> d his

     (FILE 'HOME' ENTERED AT 11:18:40 ON 21 OCT 2004)

     INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
     AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS,
     BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB,
     CROPU, DDFB, DDFU, DGENE, DISSABS, ...' ENTERED AT 11:18:52 ON 21 OCT 2004
               SEA ALPHA-CRYSTALLIN
              ---------
                5   FILE ADISCTI
                1   FILE ADISNEWS
               49   FILE AGRICOLA
                9   FILE ANABSTR
               17   FILE AQUASCI
                1   FILE BIOBUSINESS
                1   FILE BIOCOMMERCE
                7   FILE BIOENG
             1697   FILE BIOSIS
               15   FILE BIOTECHABS
               15   FILE BIOTECHDS
              689   FILE BIOTECHNO
               56   FILE CABA
               34   FILE CANCERLIT
             1550   FILE CAPLUS
                1   FILE CEABA-VTB
               22   FILE CONFSCI
                7   FILE DDFB
                6   FILE DDFU
               43   FILE DGENE
               63   FILE DISSABS
                7   FILE DRUGB
               10   FILE DRUGU
               12   FILE EMBAL
             1528   FILE EMBASE
              400   FILE ESBIOBASE
               23   FILE FEDRIP
                2   FILE FROSTI
                5   FILE FSTA
              688   FILE GENBANK
               18   FILE IFIPAT
               66   FILE JICST-EPLUS
                1   FILE KOSMET
              266   FILE LIFESCI
             1215   FILE MEDLINE
                3   FILE NIOSHTIC
                4   FILE NTIS
                4   FILE OCEAN
              350   FILE PASCAL
                8   FILE PROMT
             1500   FILE SCISEARCH
              351   FILE TOXCENTER
              134   FILE USPATFULL
                2   FILE USPAT2
               19   FILE WPIDS
               19   FILE WPINDEX
L1              QUE ALPHA-CRYSTALLIN
               ---------
```

```
     FILE 'BIOSIS, CAPLUS, EMBASE, SCISEARCH, MEDLINE, BIOTECHNO, TOXCENTER'
     ENTERED AT 11:20:17 ON 21 OCT 2004
L2          8530 S ALPHA-CRYSTALLIN
L3             1 S JAWORSKI/AU
L4             0 S L2 AND JAWORSKI
L5          2161 S ALPHA-A-CRYSTALLIN
L6             1 S L5 AND JAWORSKI

     FILE 'REGISTRY' ENTERED AT 11:23:52 ON 21 OCT 2004
L7             1 S 158856-54-3/RN
                 SET NOTICE 1 DISPLAY
                 SET NOTICE LOGIN DISPLAY

     FILE 'REGISTRY' ENTERED AT 11:24:41 ON 21 OCT 2004
                 SET TERMSET E#
                 DEL SEL Y
                 SEL L7 1 RN
L8             1 S E1/RN
                 SET TERMSET LOGIN

     FILE 'CAPLUS' ENTERED AT 11:24:45 ON 21 OCT 2004
L9             5 S L8

=> d l9 ibib ti abs 1-5

L9   ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2000:366621  CAPLUS
DOCUMENT NUMBER:          132:344010
TITLE:                    The DNA sequence of human chromosome 21
AUTHOR(S):                Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe,
                          H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishil, K.;
                          Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi,
                          T.; Sakaki, Y.; Taudlen, S.; Blechschmidt, K.; Polley,
                          A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.;
                          Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel,
                          M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh,
                          J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani,
                          A.; Sasaki, T.; Nagamine, K.; Mitsuyama, S.;
                          Antonarakis, S. E.; Minoshima, S.; Shimizu, N.;
                          Nordsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.;
                          Schon, O.; Desario, A.; Relchelt, J.; Kauer, G.;
                          Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig,
                          S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer,
                          S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis,
                          F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.
CORPORATE SOURCE:         Genomic Sciences Center, RIKEN, Sagamihara, 228-8555,
                          Japan
SOURCE:                   Nature (London) (2000), 405(6784), 311-319
                          CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER:                Nature Publishing Group
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
TI   The DNA sequence of human chromosome 21
AB   Chromosome 21 is the smallest human autosome.  An extra copy of chromosome
     21 causes Down syndrome, the most frequent genetic cause of significant
     mental retardation, which affects up to 1 in 700 live births.  Several
     anonymous loci for monogenic disorders and predispositions for common
     complex disorders have also been mapped to this chromosome, and loss of
     heterozygosity has been observed in regions associated with solid tumors.  This
     report provides the sequence and gene catalog of the long arm of
     chromosome 21.  At least 33,546,361 base pairs (bp) of DNA have been
     sequenced with very high accuracy, the largest contig being 25,491,867 bp.
```

Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be sound from the home pages of the participating centers of the chromosome 21 sequencing consortium.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:21633 CAPLUS
DOCUMENT NUMBER: 126:141113
TITLE: Cloning, expression, and chaperone-like activity of human αA-crystallin
AUTHOR(S): Andley, Usha P.; Mathur, Shashank; Griest, Terry A.; Petrash, J. Mark
CORPORATE SOURCE: Dep. Ophthalmol. Visual Sci., Washington Univ. Sch. Med., St. Louis, MO, 63110, USA
SOURCE: Journal of Biological Chemistry (1996), 271(50), 31973-31980
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

TI Cloning, expression, and chaperone-like activity of human αA-crystallin

AB One of the major protein components of the ocular lens, α-crystallin, is composed of αA and αB chain subunits that have structural homol. to the family of mammalian small heat shock proteins. Like other small heat shock proteins, α-crystallin subunits associate to form large oligomeric aggregates that express chaperone-like activity, as defined by the ability to suppress nonspecific aggregation of proteins destabilized by treatment with a variety of denaturants including heat, UV irradiation, and chemical modification. It has been proposed that age-related loss of sequences at the C terminus of the αA chain subunit may be a factor in the pathogenesis of cataract due to diminished capacity of the truncated crystallin to protect against nonspecific aggregation of lens proteins. To evaluate the functional consequences of α-crystallin modification, two mutant forms of αA subunits were prepared by site-directed mutagenesis. Like wild type (WT), aggregates of .apprx.540 kDa were formed from a tryptophan-free αA mutant (W9F). When added in stoichiometric amts., both WT and W9F subunits completely suppressed the heat-induced aggregation of aldose reductase. In contrast, subunits encoded by a truncation mutant in which the C-terminal 17 residues were deleted (R157STOP), despite having spectroscopic properties similar to WT, formed much larger aggregates with a marked reduction in chaperone-like activity. Similar results were observed when the chaperone-like activity was assessed through inhibition of γ-crystallin aggregation induced by singlet oxygen. These results demonstrate that the structurally conservative substitution of Phe for Trp-9 has a negligible effect on the functional interaction of αA subunits, and that deletion of C-terminal sequences from the αA subunit results in substantial loss of chaperone-like activity, despite overall preservation of secondary structure.

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:608 CAPLUS
DOCUMENT NUMBER: 126:102492
TITLE: Modifications of the water-insoluble human lens α-crystallins
AUTHOR(S): Lund, Anders L.; Smith, Jean B.; Smith, David L.
CORPORATE SOURCE: Dep. Chem., Univ. Nebraska, Lincoln, NE, 68588-0304, USA
SOURCE: Experimental Eye Research (1996), 63(6), 661-672
CODEN: EXERA6; ISSN: 0014-4835
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

TI Modifications of the water-insoluble human lens α-crystallins

AB Since the water-insol. crystallins of the lens may be the precursors of cataract, identifying the modifications that differentiate the water-insol. from the water-soluble crystallins may provide the basis for understanding the chemical leading to cataract. This investigation of the α-crystallins of the water-insol. urea-soluble portion of 45-yr-old normal clear lenses, isolated using gel filtration, ion exchange and reversed phase chromatog., has employed state-of-the-art mass spectrometric techniques to identify and locate the modifications of the water-insol. α-crystallins. Modifications present in the isolated α-crystallins were identified by the mol. wts. of the modified proteins, by the mol. wts. of peptides produced by enzymic digestion of the proteins, and by the fragmentation patterns produced by collisional activation of the peptides. Modifications that are either unique to the water-insol. α-crystallins or are more prevalent in the water-insol. portion than in the water-soluble part include complete oxidation of the two Cys residues of αA-crystallin to form an intramol. disulfide bond, partial truncation at both the C-termini and N-termini of αA- and αB-crystallins, partial oxidation of Met residues to methionine sulfoxide, partial deamidation of several Asn and Gln residues, and evidence of peptide bond cleavage at some of the deamidated residues. Although many reactions have been proposed to contribute to the insoly. of crystallins, this compilation of in vivo post-translational modifications of water-insol. α-crystallins delineates products that are actually present at levels of 5% or more. From these results, it is hypothesized that α-crystallin becomes water-insol. following deamidation of various Asn and Gln residues which cause conformational changes leading to formation of an intra-mol. disulfide bond between the Cys residues of αA-crystallin.

L9 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:29717 CAPLUS
DOCUMENT NUMBER: 124:280515
TITLE: A reassessment of mammalian αA-crystallin sequences using DNA sequencing: implications for anthropoid affinities of tarsier
AUTHOR(S): Jaworski, Cynthia J.
CORPORATE SOURCE: Lab. Mol. Developmental Biol., Natl. Eye Inst., Bethesda, MD, 28092, USA
SOURCE: Journal of Molecular Evolution (1995), 41(6), 901-8
CODEN: JMEVAU; ISSN: 0022-2844
PUBLISHER: Springer
DOCUMENT TYPE: Journal
LANGUAGE: English

TI A reassessment of mammalian αA-crystallin sequences using DNA sequencing: implications for anthropoid affinities of tarsier

AB αA-crystallin, a major structural protein in the ocular lenses of all vertebrates, has been a valuable tool for mol. phylogenetic studies. This paper presents the complete sequence for human αA-crystallin derived from cDNA and genomic clones. The deduced amino acid sequence

differs at two phylogenetically informative positions from that previously inferred from peptide composition This led us to examine the same region of the αA-crystallin gene in 12 other mammalian species using direct sequencing of PCR-amplified genomic DNA. New sequences were added to the database, and corrections were made to all anthropoid sequences, defining clear synapomorphies for anthropoids as a clade distinct from prosimians. Within the anthropoids there are further synapomorphies delineating hominoids, Old World monkeys, and New World monkeys. Significantly, sequence revisions and the addition of new sequence for a prosimian, the sifaka, eliminate the previous support for the proposed anthropoid affinities of the tarsier inferred from αA-crystallin protein sequences. In addition, DNA sequences provide greater resolution of certain relationships. For example, although they are identical in protein sequence, comparison of DNA sequences clearly separates mouse and the common tree shrew, grouping the tree shrew closer to prosimians. These results show that adding DNA sequences to the existing αA-crystallin database can enhance its value in resolving phylogenetic relationships.

L9 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:673440 CAPLUS
DOCUMENT NUMBER: 121:273440
TITLE: A partial cDNA sequence corrects the human αA-crystallin primary structure
AUTHOR(S): Caspers, Gert-Jan; Pennings, Jeroen; De Jong, Wilfried W.
CORPORATE SOURCE: Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB, Neth.
SOURCE: Experimental Eye Research (1994), 59(1), 125-6
CODEN: EXERA6; ISSN: 0014-4835
DOCUMENT TYPE: Journal
LANGUAGE: English
TI A partial cDNA sequence corrects the human αA-crystallin primary structure
AB The primary structure of the human αA-crystallin chain was proposed almost 20 yr ago, on the basis of peptide compns. and partial Edman degradation (de Jong et al., 1975; Kramps et al., 1978). With the advent of the DNA era, the largest part of the amino acid sequence was fully confirmed by deduction from the DNA sequences of the first two exons and the 3' end of the third exon of the human αA-crystallin gene (McDevitt et al., 1986; Jaworski and Piatigorsky, 1989). The DNA sequence of the larger part of the third exon, corresponding to positions 105-165 in the 173-residue αA-crystallin chain, still remained undetd. During the course of comparative studies of the αA-crystallin sequences of different animals, we designed two degenerate oligonucleotide primers, encompassing a region coding for amino acids 74-160. These primers were used to amplify a partial αA-crystallin cDNA sequence from a human lens cDNA library in phage λgt11 by the polymerase chain reaction (PCR) method (Saiki et al., 1985). PCR products were cloned and the sequence was determined by the dideoxynucleotide chain-termination method. The part of the nucleotide sequence of the human αA-crystallin cDNA that codes for amino acids 105-160 and its derived amino acid sequence were determined

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1215	FILE MEDLINE
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L2          8530 S ALPHA-CRYSTALLIN
L3             1 S JAWORSKI/AU
L4             0 S L2 AND JAWORSKI
L5          2161 S ALPHA-A-CRYSTALLIN
L6             1 S L5 AND JAWORSKI

     FILE 'REGISTRY' ENTERED AT 11:23:52 ON 21 OCT 2004
L7             1 S 158856-54-3/RN
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                 SET NOTICE LOGIN DISPLAY

     FILE 'REGISTRY' ENTERED AT 11:24:41 ON 21 OCT 2004
                 SET TERMSET E#
                 DEL SEL Y
                 SEL L7 1 RN
L8             1 S E1/RN
                 SET TERMSET LOGIN

     FILE 'CAPLUS' ENTERED AT 11:24:45 ON 21 OCT 2004
L9             5 S L8

     FILE 'STNGUIDE' ENTERED AT 11:25:49 ON 21 OCT 2004

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---Logging off of STN---


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FULL ESTIMATED COST                                     0.48      51.68

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